



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/676,873  
Source: OIPF  
Date Processed by STIC: 4-8-04

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

**FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221**

***Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221***

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:**

**<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

Does Not Comply  
Corrected Diskette Needed

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/676,873

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics  
    Wrapped Aminos      The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☐ Invalid Line Length      The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
- 3 ☐ Misaligned Amino  
    Numbering      The numbering under each 5<sup>th</sup> amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
- 4 ☐ Non-ASCII      The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. Please **ensure your subsequent submission is saved in ASCII text**.
- 5 ☐ Variable Length      Sequence(s) \_\_\_\_\_ contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ PatentIn 2.0  
    "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
- 7 ☐ Skipped Sequences  
    (OLD RULES)      Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for **each** skipped sequence:  
                            (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                            (i)      SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                            (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                            This sequence is intentionally skipped  
  
                            Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
- 8 ☐ Skipped Sequences  
    (NEW RULES)      Sequence(s) \_\_\_\_\_ missing. If **intentional**, please insert the following lines for **each** skipped sequence.  
                            <210> sequence id number  
                            <400> sequence id number  
                            000
- 9 ☐ Use of n's or Xaa's  
    (NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
                            Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.  
                            In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 ☒ Invalid <213>  
    Response      Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence
- 11 ☐ Use of <220>      Sequence(s) \_\_\_\_\_ missing the <220> "Feature" and associated numeric identifiers and responses.  
                            Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
                            (See "Federal Register," 07/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ PatentIn 2.0  
    "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ☐ Misuse of n/Xaa      "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid



Does Not Comply  
Corrected Diskette Needed

IFWO

## RAW SEQUENCE LISTING

DATE: 04/08/2004

PATENT APPLICATION: US/10/676,873

TIME: 07:33:37

Input Set : N:\efs\10676873\_efs\COTHP01002-usbios-S000001.txt

Output Set: N:\CRF4\04082004\J676873.raw

3 &lt;110&gt; APPLICANT: CHAN, JOHN

4 BAYNES, BRIAN

5 ZHANG, SHENGSHENG

7 <120> TITLE OF INVENTION: METHODS OF ENGINEERING SPATIALLY CONSERVED MOTIFS IN  
POLYPEPTIDES

9 &lt;130&gt; FILE REFERENCE: COTH-PO1-002

11 &lt;140&gt; CURRENT APPLICATION NUMBER: 10/676,873

12 &lt;141&gt; CURRENT FILING DATE: 2003-09-30

14 &lt;150&gt; PRIOR APPLICATION NUMBER: 60/414,688

15 &lt;151&gt; PRIOR FILING DATE: 2002-09-30

17 &lt;160&gt; NUMBER OF SEQ ID NOS: 4

19 &lt;170&gt; SOFTWARE: PatentIn version 3.2

21 &lt;210&gt; SEQ ID NO: 1

22 &lt;211&gt; LENGTH: 474

23 &lt;212&gt; TYPE: DNA

24 <213> ORGANISM: TNF alpha chain b mutation

26 &lt;400&gt; SEQUENCE: 1

27 gtcagatcat cttctcgaac ccgagtgac aagcctgtag cccatgttgt agcaaaccct 60  
 29 caagctgagg ggcagctcca gtggctgaac cgccgggcca atgccctcct ggccaatggc 120  
 31 gtggagctga gagataacca gctggtggtg ccatcagagg gcctgtacct catctactcc 180  
 33 caggtcctct tcaagggcc aagctgcccc tccacccatg tgctcctcac ccacaccatc 240  
 35 agccgcatcg cgtctccta ccagaccaag gtcaacctcc tctctgccat caagagcccc 300  
 37 tgccagaggg agaccccaga gggggctgag gccaagccct ggtatgagcc catcgatctg 360  
 39 ggaggggtct tccagctgga gaagggtgac cgactcagcg ctgagatcaa tcggcccgcac 420  
 41 tatctcgact ttgccgagtc tgggcaggtc tactttggga tcattgccct gtga 474

44 &lt;210&gt; SEQ ID NO: 2

45 &lt;211&gt; LENGTH: 157

46 &lt;212&gt; TYPE: PRT

47 <213> ORGANISM: TNF alpha protein

49 &lt;400&gt; SEQUENCE: 2

51 Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala Gly Val  
 52 1 5 10 15  
 55 Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg  
 56 20 25 30  
 59 Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu  
 60 35 40 45  
 63 Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe  
 64 50 55 60  
 67 Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Thr His Thr Ile  
 68 65 70 75 80  
 71 Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala  
 72 85 90 95  
 75 Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys  
 76 100 105 110

Please see item #10 on  
ERROR SUMMARY SHEET

- Same - see item #10

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Output Set: N:\CRF4\04082004\J676873.raw

79 Pro Gln Tyr Glu Pro Ile Asp Leu Gly Gly Val Phe Gln Leu Glu Lys  
80 115 120 125  
83 Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Leu Phe  
84 130 135 140  
87 Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu  
88 145 150 155  
91 <210> SEQ ID NO: 3  
92 <211> LENGTH: 474  
93 <212> TYPE: DNA  
94 <213> ORGANISM: TNF alpha chain c mutation — Same — see item #10  
96 <400> SEQUENCE: 3  
97 gtcagatcat cttctcgaac cccgagtgc aagcctgtag cccatgttgt agcaaaccct 60  
99 caagctgagg ggcagctcca gtggctgaac cgccgggcca atgccctcct ggccaatggc 120  
101 gtggagctga gagataacca gctgggtgtg ccatcagagg gctgtacct catcagttcc 180  
103 caggctcctct tcaagggcca aggctgcccc tccaccatg tgctcctcac ccacaccatc 240  
105 agccgcatcg ccgtctccta ccagaccaag gtcaacctcc tctctgccat caagagcccc 300  
107 tgccagaggg agaccccaga gggggtgag gccaaagcct ggtatgagcc catccatctg 360  
109 ggaggggtct tccagctgga gaagggtgac cgactcagcg ctgagatcaa tcggcccgcg 420  
111 tatctcgact ttgccgagtc tgggcaggtc tactttggga tcattgccct gtga 474  
114 <210> SEQ ID NO: 4  
115 <211> LENGTH: 157  
116 <212> TYPE: PRT  
117 <213> ORGANISM: TNF alpha protein sequence chain c — same — see item #10  
119 <400> SEQUENCE: 4  
121 Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val  
122 1 5 10 15  
125 Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg  
126 20 25 30  
129 Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu  
130 35 40 45  
133 Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Ser Ser Gln Val Leu Phe  
134 50 55 60  
137 Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Thr His Thr Ile  
138 65 70 75 80  
141 Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala  
142 85 90 95  
145 Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys  
146 100 105 110  
149 Pro Gln Tyr Glu Pro Ile His Leu Gly Gly Val Phe Gln Leu Glu Lys  
150 115 120 125  
153 Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Leu Phe  
154 130 135 140  
157 Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu  
158 145 150 155

**VERIFICATION SUMMARY**

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